OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                           No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGGCAAAAGAAATCAAATT.....TGGGTGGGATGGGCGGATAA 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               April 15, 2003, 03:00:20; Search time 314.293 Seconds (without alignments) 4571.527 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;; /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB_seq; *
;; /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq; *
;; /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB_seq; *
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/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                             Sequence 50, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 13, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 26, Appl
Sequence 26, Appl
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Sequence 29, Appl
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Sequence 21, Appl
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                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                        Sequence 50, Application US/10267311

Publication No. US20030050469A1

GENERAL INFORMATION:

APPLICANT: Siegel, Marvin

APPLICANT: Chu, N. Randall

APPLICANT: Mizzen, Lee A.

TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO

FILE REFERENCE: 12071/002001

CURRENT APPLICATION NUMBER: US/10/267,311

CURRENT FILING DATE: 2002-10-09

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION UNDER: US/09/613,757

PRIOR APPLICATION UNDER: US/09/613,757

PRIOR APPLICATION UNDER: US 60/143,757

NUMBER OF SEO ID NOS: 55

SOFTWARR: FAILING DATE: 1999-07-08

NUMBER OF SEO ID NOS: 55

SOFTWARR: FASESO FOR Windows Version 4.0

LENGTH: 1926

TYPE: DNA

ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (1)...(1923)
US-10-267-311-50
                                                                                                                                                                         Query Match 63.4%;
Best Local Similarity 77.5%;
Matches 1258; Conservative
                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: fusion sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                               1 ATGGCAAAAGAAATTAAATTTTCATCAGATGCCCGTTCAGCTATGGTCCGTGGTGTCGAT 60
                                                                                                                        1 ATGGCAAAAGAATCAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGGGGGAGTTGAT 60
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9 US-09-880-505-159
9 US-09-938-842A-2463
9 US-09-938-842A-2463
9 US-09-938-842A-2163
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9 US-10-051-643-161
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10 US-09-974-300-6303
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7 US-08-10-051-643-115
9 US-10-051-643-115
10 US-09-974-300-6301
                                                                                                                                                                       0; Mismatches 366; Indels
                                                                                                                                                                                     Score 1038.4; DB
Pred. No. 4e-244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                          DB 9; Length 1926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 159, App Sequence 151, App Sequence 113, App Sequence 113, App Sequence 174, App Sequence 1623, App Sequence 161, App Sequence 161, App Sequence 161, App Sequence 161, App Sequence 116, App Sequence 116, App Sequence 116, App Sequence 111, App Sequence 111, App Sequence 113, App Sequence 115, App Sequence 117, App Sequence 117, App Sequence 1187, App Sequence 711, App
                                                                                                                                                                       0; Gaps
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458.6 458.6 458.6 458.6 458.6 458.6 458.6 458.6

36.0 32.4 29.5 29.5 28.0 28.0 28.0 27.9 27.8 27.8

0,

Query Match

Length

SUMMARIES

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

Published_Applications_NA: *

seg length: 0

Scoring table: Sequence: Title: Perfect score:

Gapop 10.0 , Gapext 1.0

US-09-001-737-7_COPY_15_1652 1638

593429 segs, 438583890 residues

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241 241 181

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601 TACATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAATC 660
  ACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTT
                                                                                                   GCTCCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATGCT
                                                                                                                                                                                          GAAAAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGGTAGCTGTTATCAAAGTAGGA 1140
                                                                                                                                                                                                                                                                                             GCTAACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACCGT 1080
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                                                                      GCCGCAACTGAAACTGAGTTGAAAGAAATGAAACTCCGCATTGAAGATGCCCTCAACGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 42, Application US/09070927A Patent No. US20020120116A1 GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1621
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4:
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFFWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION EVINCOMN>
PRIOR APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 40,302
REFERENCE/DOCKET NUMBER: BB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
VECCHARDAM: (301) 309-8514
VECCHARDAM: (301) 309-8514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1561 AAACCAGAACCAGTAGCCCCAGCTCCAGCAATGGATCCAAGTATGATGGGTGGAATGGGC 1620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1381 ATCGTTATCGATCGTTTGAAAAATGCTGAGCTTGGTATAGGATTCAACGCAGCAACTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1261 ATTCCAGCTGTTGCTACCTTGGAATTGACAGGAGGATGAAGCAACAGGACGTAATATTGTT 1320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAG 1624
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Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.50 inch, 1.4Mb storage
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TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-070-927A-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.ATGGCAAAAGAAATCAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGAGTTGAT 60
GAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAG 960
                                          GACCGCCGCAAAGCGATGCTTGAAGATATTGCTATTTTAACAGGTGGTACAGTAATCACT 126:
                                                           GATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACA 900
                                                                                                GTATTGAACAAAATCCGTGGTACATTTAATGTTGTCGCAGTAAAAGCGCCAGGATTTGGT 120:
                                                                                                                  GTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGGGCCAGGATTTGGT 840
                                                                                                                                                       CAAAGCCGTCCACTATTGATTATTGCGGATGATGTTGATGGGGAAGCTCTACCAACATTA 1143
                                                                                                                                                                          ACCAACCGTCCATTACTCATATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTT
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                                                                                                                                                                                                                                ACGGATAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAAA 720
                                                                                                                                                                                                                                                                                                                                ATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAA 600
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Sequence 1, Application US/09790988

Patent No. US20020127687A1

GENERAL IMPORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: SAKAKI, YOSHIYUKI
ITILE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 08135/0159

FILE REFERENCE: 08135/0159

CURRENT APPLICATION NUMBER: US/09/790,988

CURRENT FILING DATE: 2001-02-23

PRIOR APPLICATION WHEER: JP2000-107160

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEO ID NOS: 7

SOFTWARE: Patentin Ver. 2.1

LENGTH. 640681
                                                                          ; ORGANISM: Buchnera US-09-790-988-1
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US-09-790-988-1
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Query Match
Best Local Similarity
Matches 991; Conserv
                                                                                                           TYPE: DNA
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                                                                                                                            640681
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                52.8%;
Score 615.8; DB 10;
Pred. No. 2.1e-139;
0; Mismatches 582;
                               Length 640681;
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19741 CAAAGTCGTATTAGTCAAATCCGACAAGAAATTCAAGAAGCTACTTCTGATTATGATAAA 19800
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                                                                                                                                                   19681 GTTGTTATTAGCAAAGACACTACAACTATTATTGGTGGTGTAGGAGAAAAACACTCCATT
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                                                                                                                                                                                                     ATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATT 1020
                                                                                                                                                                                                                                                                GAAGAATTAGCTATGGAATTAGAAAATCTACTTTAGAAGATTTAGGACAAGCAAAACGT 19680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/09960428
Patent No. US20020115147A1
GENERAL INFORMATION:
APPLICANT: Roche Diagnostics GmbH
TITLE OF INVENTION: Method for producing an active heterodimeric AMV-RT in prokary
FILE REFERENCE: 5272/09/
CURRENT APPLICATION NUMBER: US/09/960,428
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 22
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 2155
TYPE: DNA
ORGANISM: Escherichia coli
US-09-960-428-13
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US-09-960-428-13
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Best Local Similarity 61.3%;
Matches 986; Conservative
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                                                                                 598 TCTTTCGGTGCACCGACCATCACCAAAGATGGTGTTTCCGTTGCTCGTGAAATCGAACTG
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                                                                                                                                   124 GCTTTTGGTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCGAATTA 183
                                                                                                                                                                                                                                          64 TTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAGGGCGCGAATGTTGTTCTTGAAAAA 123
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Pred. No. 2.4e-134;
0; Mismatches 617; Indels 6;
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                                 ATTGAAAAGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACA---TT
                                                                                                         ACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTT 1260
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                                                                                 ACCCGTGCTGCGGTAGAAGAAGGCGTGGTTGCTGGTGGTGGTGTTGCGCTGATCCGCGTA
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Sequence 380, Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
APPLICANT: Bhatla, Ajay
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 20121.469CB
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTMARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 380
LENGTH: 1635
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
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US-09-841-132-380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 32.4%; Score 530.4; DB 10; Length 1635; Best Local Similarity 59.5%; Pred. No. 7e-120; Matches 957; Conservative 0; Mismatches 636; Indels 15;
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364 GCAACAGCAACAGCTGTTGAAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCAAGGAA 423
                                                                                                                                                                                                                                                                                                     124 GCTTTTGGTTCTCCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGAGATCGAATTA 183
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                                                                                                                                                        GATATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTCATGAA 303
                                                                                                                                                                                                                               GAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAACCAAT
                                                                                                                                                                                                                                                                            AGCTTTGGCTCTCCCCAAGTGACTAAAGATGGTGTTACTGTAGCTAAAGAAATCGAGCTC
                                                                                                                                                                                                                                                                                                                                                                       TTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTGAAAAA 123
                                                    GGTCTAAGAAATGTCACTGCCGGTGCCAATCCTATGGACCTAAAAAGAGGTATCGACAAA
                                                                                          GGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTGAAACA
                                                                                                                                GACAAAGCAGGCGACGGAACTACAACAGCAACTGTTCTTGCAGAAGCAATCTATAGCGAA
                                                                                                                                                                                                    GAAGACAAACATGAAAACATGGGCGCTCAGATGGTAAAAGAAGTCGCCAGCAAAACTGCT
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1447 TTACGTGACGCTTATACAGATATGATTGACGCAGGAATTTTAGATCCAACTAAAGTGACT 1506
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                                                                                                                                            1372 GAAGGCTCCGTAGTTATTGACAAGTTGAAAAACAGGCCTGCAGGAACAGGATTTAATGCT 1431
                                                  1432 GCAACAGGTGAGTGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACA 1491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTT 1260
                                                                                                                                                                                                                                                                                                                     ATCCCTACACTAGAAGCTTTCCTTCCTATGCTAGCAAACGAAGACGAAGCTATTGGTACT 1326
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US-08-781-986A-266
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TELEPAX: (301) 309-8512
INFORMATION FOR SEO ID NO: 266:
SEQUENCE CHARACTERISTICS:
LENGTH: 1017 base pairs
TYPE: nuclet acid
STRANDENNESS: double
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US-08-781-986A-266
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.5%; Score 483.6; DB 7; Length 1017; Best Local Similarity 67.2%; Pred. No. 1.5e-108; Matches 681; Conservative 2; Mismatches 331; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20850
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOTTWARE: ASCLI Text
CURRENT APPLICATION DATA:
APPLICATION MSDER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 266, Application US/08781986A Publication No. US20030054436A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Benson, HODER: 30,446
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB24
TELECOMMUNICATION INFORMATION:
TELECHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5255 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1567 ATCGCTGATATCCCAGAAGAGAATCTTCTTCAGCTCCAGCGATGCCA 1614:
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                                             181 TTATATTTCTGAAGCTATGGAAAAAGTAGGTAACGATGGTGTCATTACAATTGAAGAATC
534 TCGAGGTATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCT 593
                                                                                          474 GTATATCTCAGAAGCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATC 533
                                                                                                                                          121 AAATAAAATGAAATTGCGCAAGTAGGTGCGATTTCAGCAGCAGCAGAAAATTGGACG 180
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                                                                                                                                                                                                                                                                                        354 CATTGAAACAGCAACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATC 413
                                                                                                                                                                                                                                          61 TATCGACAAAGCAGTTAAAGTTGCTGTTGAAGCGTTACATGAAAATTCTCAAAAAGTTGA 120
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STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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RESULT 7
US-09-738-626-665
Sequence 665, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                           APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATELSHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                  APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROS
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: CCHIAI, KEIKO
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
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PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 665
LENGTH: 1614
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-665
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CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION UNMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION UNMBER: 60/179,531
PRIOR FILING DATE: 2000-02-01
PRIOR APPLICATION UNMBER: 60/117,844
PRIOR APPLICATION UNMBER: 60/117,844
PRIOR APPLICATION UNMBER: 60/118,206,
PRIOR APPLICATION UNMBER: 60/118,206,
PRIOR APPLICATION UNMBER: 60/118,206,
PRIOR APPLICATION UNMBER: 60/118,206,
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US-09-712-363-23
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23, Application US/09712363 Patent No. US20020164588A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                              APPLICANT: Eisenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS
FILE REFERENCE: 07419-032001
FILE REFERENCE: 07419-032001
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1561 GTTGAGAAGCCTGCAGAAG 1579
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PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION UNBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION UNBER: 60/143,092
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 23
SEQ ID NO 23
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
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Best Local Similarity 55.8
Conservative
                              721 ACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTT 780
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                                                                                                    661 GTCAGCTCCAAGGTGTCCACTGTCAAGGATCTGCTGCCGCTGCTCGAGAAGGTCATCGGA 720
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Sequence 3, Application US/10267311

Publication No. US20030050469A1

GENERAL INFORMATION:

APPLICANT: Siegel, Marvin

APPLICANT: Chu, N. Randall

APPLICANT: Mizzen, Lee A.

TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO

FILE REFERENCE: 12071/002001

CURRENT APPLICATION NUMBER: US/10/267,311

CURRENT FILING DATE: 2002-10-09

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR APPLICATION NUMBER: US 60/143,757
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; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-10-267-311-3
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NUMBER OF SEC ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEC ID NO 3
LENGTH: 1623
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Best Local Similarity
Matches 875; Conserv
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
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                                                                                            ACCAACCGTCCATTACTCATTATTGCAGATGATGATGGTGAAGCACTTCCAACCCTT
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Pred. No. 2.6e-102;
0; Mismatches 694;
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-07-08
VINDBER OF SEQ ID NOS: 55
SOFTMARE: FastSEQ for Windows Version 4.0
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; LOCATION: (1)...(1917)
US-10-267-311-16
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Best Local Similarity 55.8%;
Matches 875; Conservative
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion sequence
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RESULT 10 US-10-267-311-16

Sequence 16, Application US/10267311 Publication No. US20030050469A1 GENERAL INFORMATION:

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Sequence 28, Application US/10267311

Publication No. US20030050469A1

GENERAL INFORMATION:

APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall

APPLICANT: Chu, N. Randall

APPLICANT: MIZZEN, Lee A,

FILE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO

FILE REFERENCE: 12071/002001

CURRENT FILING DATE: 2002-10-09

PRIOR APPLICATION NUMBER: US/10/267,311

CURRENT FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: US 60/143,757

PRIOR FILING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 55

NUMBER OF SEQ ID NOS: 55

LENGTHARE: PASTSEQ for Windows Version 4.0

SEQ ID NO 28

LENGTH: 1947

TYPE: DNA
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US-10-267-311-28
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ORGANISM: Artificial Sequence
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: NAME/KEY: CDS; LOCATION: (1)...(1944)
US-10-267-311-28
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Best Local Similarity 55.8%;
Matches 875; Conservative
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                             901 GAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTTGGACAGGCCTGCTAAG 960
                                                                                                                                                                                                                                                                              721 ACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTT 780
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                                                                           GACCGCCGCAAGGCGATGCTGCAGGATATGGCCATTCTCACCGGTGGTCAGGTGATCAGC
                                                                                                  GATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACA 900
                                                                                                                                                                                                                                                                                                                   GTCAGCTCCAAGGTGTCCACTGTCAAGGATCTGCTGCCGCTGCTCGAGAAGGTCATCGGA 1044
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Pred. No. 2.8e-102;
0; Mismatches 694;
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US-10-267-311-20

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RESULT 12

US-10-267-311-20

Sequence 20, Application US/10267311

Publication No. US20030050469A1

GENERAL INFORMATION:

APPLICANT: Siegel, Marvin
APPLICANT: Siegel, Marvin
APPLICANT: Mizzen, Lee A.

TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001

CURRENT APPLICATION NUMBER: US/10/267,311

CURRENT FILING DATE: 2002-10-09

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR FILING DATE: 1999-07-08

UNBBER OF SEQ ID NOS: 55

SOFTMARE: FRASTSEQ for Windows Version 4.0

SEQ ID NO 20

LENGTH: 2847

TYPE: DNA
ORGANISM: Artificial Sequence
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1021 GTCGTGGTCACCAAGGACGAGACCACCATCGTCGAGGGCGCCGGTGACACCGACGCCATC 1080
                                                                                                                                                                                                                       961 ATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATT 1020
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FEATURE:
OTHER INFORMATION: fusion sequence

NAME/KEY: CDS LOCATION: (1) ...(2844)

US-09-738-626-2986

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FILE REFERENCE: 249-125
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1900-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ 1D NOS: 7059
SOFTWARE: Patentin ver. 3.0
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US-09-738-626-2986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2986, Application US/09738626 Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                   APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
ORGANISM: Corynebacterium glutamicum
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961 GGCCAGGCACGCAAGGTTGTTGTCACCAAGGATGACACCACCATCGTTGACGGCGCAGGT 1020
                                946 GGACAGGCTGCTAAGATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGA 1005
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                                                                                                  886 GGTACAGTGATTACAGAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTT 945
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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 90/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NOS: 7059
SEQ ID NO 1
SEQ ID NO 1
FENGTH - 22040
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US-09-738-626-1/c
US-09-738-626-1/c
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
      TYPE: DNA
ORGANISM: Corynebacterium glutamicum
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2889580 GGCCAGGCACGCAAGGTTGTTGTCACCAAGGATGACACCACCATCGTTGACGGCGCAGGT 2889521
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Best Local Similarity 56.4
Matches 903; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2889820 GAGAAGGTCATGCAGTCCGGCAAGCCTTTGCTGATCATCTCTGAGGACGTCGAGGGCGAG 2889761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2889940 GGCTACATCTCCGGTTACTTCGCAACTGACATGGAGCGCCTCGAGGCTGTTCTGGAAGAT 2889881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2890360 CTTGAGGATCCTTACGAGAAGATCGGCGCAGAGCTGGTCAAGGAAGTCGCTAAGAAGACT 2890301
                                                      946 GGACAGGCTGCTAAGATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGA 1005
                                                                                                                                                      886 GGTACAGTGATTACAGAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTT 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 TCAGAAGCTATGGAGCGTGTGGG-------CAACGATGGTGTGATTACCATC 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 GAAGCTATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATATC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 ACAGCAACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCAAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 GAAGGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTGAA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AATGATATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTCAT 300
                                                                                                                                                                                                                                                                                                                                                                                          646 CCATTTATCTTAATCACGGATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTT 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        586 GGTTACCTGTCTCAATACATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAAC 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        526 GAAGAATCTCGAGGTATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGT 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TTAGAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAACC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AAAGCTTTTGGTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCGAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ATGTTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGGCAAAAGAAATCAAATTTTCAGCAGATGCGGGTGCTGCCATGGTGCGGGAGTTGAT 60
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Pred. No. 3.4e-100;
0; M1smatches 680; Indels 18;
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SEIKO

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Sequence 9, Application US/10068059
Patent No. US20020155434A1
GENERAL INFORMATION:
APPLICANT: MIZZEN, Lee A.
APPLICANT: HONGWel, Liu
APPLICANT: Siegel, Marvin
TITLE OF INVENTION: HEPATITIS B VIRUS TREATMENT
FILE REFERENCE: 1207-107002
CURRENT APPLICATION NUMBER: US/10/068,059
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 60/266,733
PRIOR APPLICATION UNDER: US/10/266,733
PRIOR FILING DATE: 2001-02-05
UNDBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 2073
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: Cor
              Ş
                                                                                                                                                                 ; NAME/RBY: CDS

; LOCATION: (1)...(2070)

; OTHER INFORMATION: Nucleic acids encoding fusion protein

US-10-068-059-9
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US-10-068-059-9
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                                                               Best Local Similarity Matches 872; Conserv
                                                                                   Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2889280 GCGCTGCTGCAGGCTGCTCACGTCCTGGACAACGATCTTGAGCTTTCCGGCGACGAGGCA 2889221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1126 GTTATCAAAGTAGGAGCTCCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGGATTGAG 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1483 AAAGTAACACGATCAGGGCTTCAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACA 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1363 GCTGGGTAGGAAGGCTCCGTAGTTATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGA 1422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1186 GATGCTCTAAATGCTACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGGAACA 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1423 TTTAATGCTGCAACAGGTGAGTGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTC 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1303 ACTGGACGTAACATTGTGCTTCGTGCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAAT 1362
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4 GCAAAAGAAATCAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGAGTTGATATG 63
                                                               Conservative
                                                                                   27.8%;
55.7%;
                                              0; Mismatches 694; Indels 0;
                                                                                   Score 455.6; DB 9;
Pred. No. 1.6e-101;
                                                                                                    Length
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1084 AAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTGGTGTTATCAAAGTAGGAGCT 1143
                                                              1474 GGACGAGTGGCCCAGATCCGCCAGGAGATCGAGAACAGCGACTCCGACTACGACCGTGAG
                                                                                            1024 AACCGTATTGCACTGATTAAATCGCAATTAGAAACAACTTCTGACTTTGACGGTGAA 1083
                                                                                                                                                    1414 GTGGTCACCAAGGACGAGACCACCATCGTCGAGGGCGCCGGTGACACCGACGCCATCGCC
                                                                                                                                                                                                                                         1354 GAGGTCGGCCTGACGCTGGAGAACGCCGACCTGTCGCTAGGCAAGGCCCCGCAAGGTC 1413
                                                                                                                                                                                                                                                                                                                            1294 CGCCGCAAGGCGATGCTGCAGGATATGGCCATTCTCACCGGTGGTCAGGTGATCAGCGAA 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1174 GGTAAGCCGCTGCTGATCATCGCCGAGGACGTCGAGGGCGAGGCGCTGTCCACCCTGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                               1234 GTCAACAAGATCCGCGGCACCTTCAAGTCGGTGGCGGTCAAGGCTCCCGGCTTCGGCGAC 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1114 AGCTCCAAGGTGTCCACTGTCAAGGATCTGCTGCCGCTGCTCGAGAAGGTCATCGGAGCC 1173
                                                                                                                                                                               964 ACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATTGCT 1023
                                                                                                                                                                                                                                                                                 904 GATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAGATT 963
                                                                                                                                                                                                                                                                                                                                                                       844 CGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACAGAG 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                  784 TTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGGCCAGGATTTGGTGAT 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               724 AACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             664 GATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAAAACC 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484 GAAGCTATGGACGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAGGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             874 CAGATTGCGGCCACCGCAGCGATTTCGGCGGTGACCAGTCCATCGGTGACCTGATCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 GCTATTGCTCAGGTCGCTGCAGTATCACGCTCTGAAAAAGTTGGAGAGTATATCTCA 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 GCAACAGCAACAGCTGTTGAAGCCTTTGAAAGCCATTGCTCAACCTGTATCTGGCAAGGAA 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           694 GACGTCGCCGGTGACGGCACCACGACGGCCCACCGTGCTGGCCCAGGCGTTGGTTCGCGAG 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 GATATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTCATGAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                634 GAGGATCCGTACGAGAAGATCGGCGCCGAGCTGGTCAAAGAGGTAGCCAAGAAGACCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTTTGGTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCGAATTA
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AAGCTGCAGGAGCGGCTGGCCAAAGCTGGCCGTGATCAAGGCCGGTGCC 1593 CCAACAGAGACAACTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATGCTACA 1203 I

Search completed: April 15, 2003, 09:09:26 Job time : 3195.29 secs